



SEQUENCE LISTING

<110> Hotten, Gertrud
Neidhardt, Helge
Paulista, Michael

<120> NEW GROWTH/DIFFERENTIATING FACTOR OF TGF- FAMILY

<130> 100564-09022

<140> US 09/386,450

<141> 1999-08-31

<150> US 08/288,508

<151> 1994-08-10

<150> DE P 43 26 829.3

<151> 1993-08-10

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<151> 1994-05-25

<150> DE P 44 20 157.5

<151> 1994-06-09

<160> 41

<170> PatentIn version 3.0

<210> 1

<211> 2703

<212> DNA

<213> Artificial/Unknown

<220>

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<222> (1)..(2703)

<223> coding region for TGF-beta protien MP-52

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<210> 2

<211> 501

<212> PRT

<213> Artificial/Unknown

<220>

<221> DOMAIN

<222> (1)..(501)

<223> TGF-beta protien MP-52

<400> 2

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Leu	Asp	Leu	Glu	Phe	Ile	Cys	Thr	Val	Leu	Gly	Ala	Pro	Asp	Leu	Gly
		20						25					30		
Gln	Arg	Pro	Gln	Gly	Thr	Arg	Pro	Gly	Leu	Ala	Lys	Ala	Glu	Ala	Lys
		35					40					45			
Glu	Arg	Pro	Pro	Leu	Ala	Arg	Asn	Val	Phe	Arg	Pro	Gly	Gly	His	Ser
	50					55					60				
Tyr	Gly	Gly	Gly	Ala	Thr	Asn	Ala	Asn	Ala	Arg	Ala	Lys	Gly	Gly	Thr
65					70					75					80
Gly	Gln	Thr	Gly	Gly	Leu	Thr	Gln	Pro	Lys	Lys	Asp	Glu	Pro	Lys	Lys
			85						90					95	
Leu	Pro	Pro	Arg	Pro	Gly	Gly	Pro	Glu	Pro	Lys	Pro	Gly	His	Pro	Pro
			100					105					110		
Gln	Thr	Arg	Gln	Ala	Thr	Ala	Arg	Thr	Val	Thr	Pro	Lys	Gly	Gln	Leu
		115					120						125		
Pro	Gly	Gly	Lys	Ala	Pro	Pro	Lys	Ala	Gly	Ser	Val	Pro	Ser	Ser	Phe
	130						135				140				
Leu	Leu	Lys	Lys	Ala	Arg	Glu	Pro	Gly	Pro	Pro	Arg	Glu	Pro	Lys	Glu
145					150					155					160
Pro	Phe	Arg	Pro	Pro	Pro	Ile	Thr	Pro	His	Glu	Tyr	Met	Leu	Ser	Leu
				165					170					175	
Tyr	Arg	Thr	Leu	Ser	Asp	Ala	Asp	Arg	Lys	Gly	Gly	Asn	Ser	Ser	Val
		180						185					190		
Lys	Leu	Glu	Ala	Gly	Leu	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Ile	Asp	Lys
		195					200					205			
Gly	Gln	Asp	Asp	Arg	Gly	Pro	Val	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe
		210				215					220				

Asp Ile Ser Ala Leu Glu Lys Asp Gly Leu Leu Gly Ala Glu Leu Arg
 225 230 235 240
 Ile Leu Arg Lys Lys Pro Ser Asp Thr Ala Lys Pro Ala Ala Pro Gly
 245 250 255
 Gly Gly Arg Ala Ala Gln Leu Lys Leu Ser Ser Cys Pro Ser Gly Arg
 260 265 270
 Gln Pro Ala Ser Leu Leu Asp Val Arg Ser Val Pro Gly Leu Asp Gly
 275 280 285
 Ser Gly Trp Glu Val Phe Asp Ile Trp Lys Leu Phe Arg Asn Phe Lys
 290 295 300
 Asn Ser Ala Gln Leu Cys Leu Glu Leu Glu Ala Trp Glu Arg Gly Arg
 305 310 315 320
 Ala Val Asp Leu Arg Gly Leu Gly Phe Asp Arg Ala Ala Arg Gln Val
 325 330 335
 His Glu Lys Ala Leu Phe Leu Val Phe Gly Arg Thr Lys Lys Arg Asp
 340 345 350
 Leu Phe Phe Asn Glu Ile Lys Ala Arg Ser Gly Gln Asp Asp Lys Thr
 355 360 365
 Val Tyr Glu Tyr Leu Phe Ser Gln Arg Arg Lys Arg Arg Ala Pro Leu
 370 375 380
 Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys
 385 390 395 400
 Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp Asp Asp
 405 410 415
 Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Leu
 420 425 430
 Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Val
 435 440 445
 Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr
 450 455 460
 Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp
 465 470 475 480
 Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu
 485 490 495
 Ser Cys Gly Cys Arg
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<210> 3

<211> 24

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(24)

<223> MP-52 adapter primer

<400> 3
agaattcgca tgccatgggc gacg

24

<210> 4

<211> 23

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(23)

<223> MP-52 internal primer

<400> 4
cttgagtacg aggctttcca ctg

23

<210> 5

<211> 24

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(24)

<223> MP-52 adapter primer

<400> 5
attcgcatgc catggtcgac gaag

24

<210> 6

<211> 23

<212> DNA

<213> Artificial/Unknown

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<221> misc_feature

<222> (1)..(23)

<223> MP-52 internal primer

<400> 6
ggagcccacg aatcatgcag tca

23

<210> 7

<211> 23

<212> DNA

<213> Artificial/Unknown

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<221> misc_feature

<222> (1)..(23)

<223> MP-52 internal primer

<400> 7
acagcaggtg ggtggtgtgg act

23

<210> 8

<211> 44

<212> DNA

<213> Artificial/Unknown

<220>

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<222> (1)..(44)

<223> adapter sequece

<400> 8
agaattcgca tgccatggtc gacgaagctt tttttttttt tttt

44

<210> 9

<211> 20

<212> DNA

<213> Artificial/Unknown

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<221> misc_feature

<222> (1)..(20)

<223> MP-52 internal primer

<400> 9
ccagcagccc atccttctcc

20

<210> 10

<211> 24

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(24)

<223> MP-52 internal primer

<400> 10
tccagggcac taatgtcaaa cacg

24

<210> 11

<211> 24

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(24)

<223> MP-52 internal primer

<400> 11
actaatgtca aacacgtacc tctg

24

<210> 12

<211> 10

<212> DNA

<213> Artificial/Unknown

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<221> misc_feature

<222> (1)..(10)

<223> adapter

<400> 12
agcggccgct

10

<210> 13

<211> 102

<212> PRT

<213> Artificial/Unknown

<220>

<221> DOMAIN

<222> (1)..(102)

<223> MP-52

<400> 13

Cys	Ser	Arg	Lys	Ala	Leu	His	Val	Asn	Phe	Lys	Asp	Met	Gly	Trp	Asp
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Asp	Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Phe	His	Cys	Glu	Gly
		20					25						30		
Leu	Cys	Glu	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala
		35					40					45			
Val	Ile	Gln	Thr	Leu	Met	Asn	Ser	Met	Asp	Pro	Glu	Ser	Thr	Pro	Pro
		50				55				60					
Thr	Cys	Cys	Val	Pro	Thr	Arg	Leu	Ser	Pro	Ile	Ser	Ile	Leu	Phe	Ile
65					70					75					80
Asp	Ser	Ala	Asn	Asn	Val	Val	Tyr	Lys	Gln	Tyr	Glu	Asp	Met	Val	Val
			85						90					95	
Glu	Ser	Cys	Gly	Cys	Arg										
			100												

<210> 14

<211> 101

<212> PRT

<213> Artificial/Unknown

<220>

<221> DOMAIN

<222> (1)..(101)

<223> portion of BMP 2 corresponding to MP 52

<400> 14

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
1 5 10 15

Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly
20 25 30

Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
35 40 45

Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala
50 55 60

Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
65 70 75 80

Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu
85 90 95

Gly Cys Gly Cys Arg
100

<210> 15

<211> 101

<212> PRT

<213> Artificial/Unknown

<220>

<221> DOMAIN

<222> (1)..(101)

<223> portion of BMP 4 corresponding to MP 52

<400> 15

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
1 5 10 15
Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly
20 25 30
Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
35 40 45
Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala
50 55 60
Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
65 70 75 80
Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu
85 90 95
Gly Cys Gly Cys Arg
100

<210> 16

<211> 102

<212> PRT

<213> Artificial/Unknown

<220>

<221> DOMAIN

<222> (1)..(102)

<223> portion of BMP 5 corresponding to MP 52

<400> 16

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1 5 10 15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
20 25 30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
12

35	40	45
Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys		
50	55	60
Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe		
65	70	75
Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val		
85	90	95
Arg Ser Cys Gly Cys His		
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<210> 17

<211> 102

<212> PRT

<213> Artificial/Unknown

<220>

<221> DOMAIN

<222> (1)..(102)

<223> portion of BMP 6 corresponding to MP 52

<400> 17

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln		
1	5	10
Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly		
20	25	30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala		
35	40	45
Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys		
50	55	60
Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe		
65	70	75
Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val		
85	90	95
Arg Ala Cys Gly Cys His		
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<210> 18

<211> 102

<212> PRT

<213> Artificial/Unknown

<220>

<221> DOMAIN

<222> (1)..(102)

<223> portion of BMP 7 corresponding to MP 52

<400> 18

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1 5 10 15

Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
20 25 30

Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala
35 40 45

Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys
50 55 60

Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr Phe
65 70 75 80

Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
85 90 95

Arg Ala Cys Gly Cys His
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<210> 19

<211> 36

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(36)

<223> primer OD

<400> 19
atgaattccc atggacctgg gctggmakga mtggat

36

<210> 20

<211> 22

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(22)

<223> portion of BMP 2 corresponding to primer OD

<400> 20
acgtggggtg gaatgactgg at

22

<210> 21

<211> 22

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(22)

<223> portion of BMP 3 corresponding to primer OD

<400> 21
atattggctg gagtgaatgg at

22

<210> 22

<211> 22

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(22)

<223> portion of BMP 4 corresponding to primer OD

<400> 22

atgtgggctg gaatgactgg at

22

<210> 23

<211> 22

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(22)

<223> portion of BMP 7 corresponding to primer OD

<400> 23

acctgggctg gcaggactgg at

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<210> 24

<211> 22

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(22)

<223> portion of TGF-beta-1 corresponding to primer OD

<400> 24
aggacctcgg ctggaagtgg at

22

<210> 25

<211> 22

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(22)

<223> portion of TGF-beta-2 corresponding to primer OD

<400> 25
gggatctagg gtggaaatgg at

22

<210> 26

<211> 22

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(22)

<223> portion of TGF-beta-3 corresponding to primer OD

<400> 26
aggatctggg ctggaagtgg gt

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<210> 27

<211> 22

<212> DNA

<213> Artificial/Unknown

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<221> misc_feature

<222> (1)..(22)

<223> portion of Inhibin alpha corresponding to primer OD

<400> 27
agctgggctg ggaacggtgg at

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<210> 28

<211> 22

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(22)

<223> portion of Inhibin beta-gamma corresponding to primer OD

<400> 28
acatcggctg gaatgactgg at

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<210> 29

<211> 22

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(22)

<223> portion of Inhibin beta-beta corresponding to primer OD

<400> 29
tcatcggctg gaacgactgg at

22

<210> 30

<211> 29

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(29)

<223> Primer OID

<400> 30
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29

<210> 31

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(21)

<223> portion of BMP 2 corresponding to primer OID

<400> 31
gagttctgtc gggacacagc a

21

<210> 32

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(21)

<223> portion of BMP 3 corresponding to primer OID

<400> 32
catcttttct ggtacacagc a

21

<210> 33

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(21)

<223> portion of BMP 4 corresponding to primer OID

<400> 33
cagttcagtg ggcacacaac a

21

<210> 34

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(21)

<223> portion of BMP 7 corresponding to primer OID

<400> 34
gagctgcgtg ggcgcacagc a

21

<210> 35

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(21)

<223> portion of TGF-beta-1 corresponding to primer OID

<400> 35
cagcgcctgc ggcacgcagc a

21

<210> 36

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(21)

<223> portion of TGF-beta-2 corresponding to primer OID

<400> 36
taaattcttgg gacacgcagc a

21

<210> 37

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(21)

<223> portion of TGF-beta-3 corresponding to primer OID

<400> 37
caggtcctgg ggcacgcagc a

21

<210> 38

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(21)

<223> portion of Inhibin alpha corresponding to primer OID

<400> 38

ccctgggaga gcagcacagc a

21

<210> 39

<211> 21

<212> DNA

<213> Artificial/Unknown

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<221> misc_feature

<222> (1)..(21)

<223> portion of Inhibin beta-gamma corresponding to primer OID

<400> 39

cagcttggtg ggcacacagc a

21

<210> 40

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(21)

<223> portion of Inhibin beta-beta corresponding to primer OID

<400> 40
cagcttggtg ggaatgcagc a

21

<210> 41

<211> 10

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> (1)..(10)

<223> Adapter

<400> 41
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10